* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page for STN Seminar Schedule - N. America
NEWS 2	DEC 01	ChemPort single article sales feature unavailable
NEWS 3	FEB 02	Simultaneous left and right truncation (SLART) added for CERAB, COMPUAB, ELCOM, and SOLIDSTATE
NEWS 4	FEB 02	GENBANK enhanced with SET PLURALS and SET SPELLING
NEWS 5	FEB 06	Patent sequence location (PSL) data added to USGENE
NEWS 6	FEB 10	COMPENDEX reloaded and enhanced
NEWS 7	FEB 11	WTEXTILES reloaded and enhanced
NEWS 8	FEB 19	New patent-examiner citations in 300,000 CA/CAplus patent records provide insights into related prior art
NEWS 9	FEB 19	Increase the precision of your patent queries -- use terms from the IPC Thesaurus, Version 2009.01
NEWS 10	FEB 23	Several formats for image display and print options discontinued in USPATFULL and USPAT2
NEWS 11	FEB 23	MEDLINE now offers more precise author group fields and 2009 MeSH terms
NEWS 12	FEB 23	TOXCENTER updates mirror those of MEDLINE - more precise author group fields and 2009 MeSH terms
NEWS 13	FEB 23	Three million new patent records blast AEROSPACE into STN patent clusters
NEWS 14	FEB 25	USGENE enhanced with patent family and legal status display data from INPADOCDB
NEWS 15	MAR 06	INPADOCDB and INPAFAMDB enhanced with new display formats
NEWS 16	MAR 11	EPFULL backfile enhanced with additional full-text applications and grants
NEWS 17	MAR 11	ESBIOBASE reloaded and enhanced
NEWS 18	MAR 20	CAS databases on STN enhanced with new super role for nanomaterial substances
NEWS 19	MAR 23	CA/CAplus enhanced with more than 250,000 patent equivalents from China
NEWS 20	MAR 30	IMSPATENTS reloaded and enhanced
NEWS 21	APR 03	CAS coverage of exemplified prophetic substances enhanced
NEWS 22	APR 07	STN is raising the limits on saved answers
NEWS 23	APR 24	CA/CAplus now has more comprehensive patent assignee information
NEWS 24	APR 26	USPATFULL and USPAT2 enhanced with patent assignment/reassignment information
NEWS 25	APR 28	CAS patent authority coverage expanded
NEWS 26	APR 28	ENCOMPLIT/ENCOMPLIT2 search fields enhanced
NEWS 27	APR 28	Limits doubled for structure searching in CAS REGISTRY

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS LOGIN Welcome Banner and News Items

Enter NEWS followed by the item number or name to see news on that specific topic.

products is prohibited and may result in loss of user privileges
and other penalties.

* * * * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:56:11 ON 29 APR 2009

=> file caplus biosis
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 0.22 0.22

FILE 'CAPLUS' ENTERED AT 11:56:46 ON 29 APR 2009
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'BIOSIS' ENTERED AT 11:56:46 ON 29 APR 2009
Copyright (c) 2009 The Thomson Corporation

=> ISCOMATRIX
L1 102 ISCOMATRIX

=> HCV
L2 45943 HCV

=> L1 and L2
L3 4 L1 AND L2

=> D L3 IBIB ABS 1-4

L3 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Citing References

ACCESSION NUMBER: 2008:880662 CAPLUS
DOCUMENT NUMBER: 149:150269
TITLE: Induction of broad CD4+ and CD8+ T-cell responses and cross-neutralizing antibodies against hepatitis C virus by vaccination with Th1-adjuvanted polypeptides followed by defective alphaviral particles expressing envelope glycoproteins gpE1 and gpE2 and nonstructural proteins 3, 4, and 5
AUTHOR(S): Lin, Yinling; Kwon, Taewoo; Polo, John; Zhu, Yi-Fei; Coates, Stephen; Crawford, Kevin; Dong, Christine; Wininger, Mark; Hall, John; Selby, Mark; Coit, Doris; Medina-Selby, Angelica; McCoin, Colin; Ng, Philip; Drane, Debbie; Chien, David; Han, Jang; Vajdy, Michael; Houghton, Michael
CORPORATE SOURCE: Novartis Vaccine and Diagnostic, Inc., Emeryville, CA, 94608, USA
SOURCE: Journal of Virology (2008), 82(15), 7492-7503
CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Broad, multispecific CD4+ and CD8+ T-cell responses to the hepatitis C virus (**HCV**), as well as virus-cross-neutralizing antibodies, are assocd. with recovery from acute infection and may also be assocd. in chronic **HCV** patients with a favorable response to antiviral treatment. In order to recapitulate all of these responses in an ideal vaccine regimen, we

have explored the use of recombinant **HCV** polypeptides combined with various Th1-type adjuvants and replication-defective alphaviral particles encoding **HCV** proteins in various prime/boost modalities in BALB/c mice. Defective chimeric alphaviral particles derived from the Sindbis and Venezuelan equine encephalitis viruses encoding either the **HCV** envelope glycoprotein gpE1/gpE2 heterodimer (E1E2) or nonstructural proteins 3, 4, and 5 (NS345) elicited strong CD8+ T-cell responses but low CD4+ T helper responses to these **HCV** gene products. In contrast, recombinant E1E2 glycoproteins adjuvanted with MF59 contg. a CpG oligonucleotide elicited strong CD4+ T helper responses but no CD8+ T-cell responses. A recombinant NS345 polyprotein also stimulated strong CD4+ T helper responses but no CD8+ T-cell responses when adjuvanted with **Iscomatrix** contg. CpG. Optimal elicitation of broad CD4+ and CD8+ T-cell responses to E1E2 and NS345 was obtained by first priming with Th1-adjuvanted proteins and then boosting with chimeric, defective alphaviruses expressing these **HCV** genes. In addn., this prime/boost regimen resulted in the induction of anti-E1E2 antibodies capable of cross-neutralizing heterologous **HCV** isolates in vitro. This vaccine formulation and regimen may therefore be optimal in humans for protection against this highly heterogeneous global pathogen.

L3 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:943250 CAPLUS
DOCUMENT NUMBER: 146:106962
TITLE: The **ISCOMATRIX** adjuvant
AUTHOR(S): Drane, Debbie; Pearse, Martin J.
CORPORATE SOURCE: CSL Limited, Parkville, Australia
SOURCE: Immunopotentiators in Modern Vaccines (2006), 191-215. Editor(s): Schijns, Virgil E. J. C.; O'Hagan, Derek T. Elsevier Inc.: Burlington, Mass. CODEN: 69IKTO; ISBN: 978-0-12-088403-2
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review. **ISCOMATRIX** adjuvant is essentially the same structure as the ISCOM vaccine but without the incorporated antigen. Antigens can be formulated with the **ISCOMATRIX** adjuvant to produce **ISCOMATRIX** vaccines which provide the same antigen presentation and immunomodulatory properties as ISCOM vaccines but much broader application. **ISCOMATRIX** vaccines are safe and well tolerated in humans with no vaccine-related serious adverse events or clin. significant lab. abnormalities reported. **ISCOMATRIX** vaccines are capable of inducing strong humoral responses with increases in the magnitude, speed, and longevity of the responses, as well as the capacity for antigen dose redn. when compared to other adjuvants such as aluminum. The properties of **ISCOMATRIX** vaccines make them viable candidates for the further development and registration of prophylactic and therapeutic human vaccines.

REFERENCE COUNT: 87 THERE ARE 87 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2001:167132 CAPLUS
DOCUMENT NUMBER: 134:324893
TITLE: Characterization of hepatitis C virus core-specific immune responses primed in rhesus macaques by a nonclassical ISCOM vaccine
AUTHOR(S): Polakos, Noelle K.; Drane, Debbie; Cox, John; Ng,

Philip; Selby, Mark J.; Chien, David; O'Hagan, Derek T.; Houghton, Michael; Paliard, Xavier
CORPORATE SOURCE: Chiron Corp., Emeryville, CA, 94608, USA
SOURCE: Journal of Immunology (2001), 166(5), 3589-3598
CODEN: JOIMA3; ISSN: 0022-1767
PUBLISHER: American Association of Immunologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Current therapies for the treatment of hepatitis C virus (**HCV**) infection are only effective in a restricted no. of patients. Cellular immune responses, particularly those mediated by CD8+ CTLs, are thought to play a role in the control of infection and the response to antiviral therapies. Because the Core protein is the most conserved **HCV** protein among genotypes, the authors evaluated the ability of a Core prototype vaccine to prime cellular immune responses in rhesus macaques. Since there are serious concerns about using a genetic vaccine encoding for Core, this vaccine was a non-classical ISCOM formulation in which the Core protein was adsorbed onto (not entrapped within) the **ISCOMATRIX**, resulting in ~1-μm particulates (as opposed to 40 nm for classical ISCOM formulations). The authors report that this Core-ISCOM prototype vaccine primed strong CD4+ and CD8+ T cell responses. Using intracellular staining for cytokines, the authors show that in immunized animals 0.30-0.71 and 0.32-2.21% of the circulating CD8+ and CD4+ T cells, resp., were specific for naturally processed **HCV** Core peptides. Furthermore, this vaccine elicited a Th0-type response and induced a high titer of Abs against Core and long-lived cellular immune responses. Finally, the authors provide evidence that Core-ISCOM could serve as an adjuvant for the **HCV** envelope protein E1E2. Thus, these data provide evidence that Core-ISCOM is effective at inducing cellular and humoral immune responses in nonhuman primates.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

Full Text | Cited References

ACCESSION NUMBER: 2009:93260 BIOSIS
DOCUMENT NUMBER: PREV200900093260
TITLE: Induction of broad CD4(+) and CD8(+) T-cell responses and cross-neutralizing antibodies against hepatitis C virus by vaccination with Th1-adjuvanted polypeptides followed by defective alphaviral particles expressing envelope glycoproteins gpE1 and gpE2 and nonstructural proteins 3, 4, and 5.
AUTHOR(S): Lin, Yinling [Reprint Author]; Kwon, Taewoo; Polo, John; Zhu, Yi-Fei; Coates, Stephen; Crawford, Kevin; Dong, Christine; Wininger, Mark; Hall, John; Selby, Mark; Coit, Doris; Medina-Selby, Angelica; McCoin, Colin; Ng, Philip; Drane, Debbie; Chien, David; Han, Jang; Vajdy, Michael; Houghtont, Michael
CORPORATE SOURCE: 4 Captain Dr 411, Emeryville, CA 94608 USA
yinlilin918@yahoo.com
SOURCE: Journal of Virology, (AUG 2008) Vol. 82, No. 15, pp. 7492-7503.
CODEN: JOVIAM. ISSN: 0022-538X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Jan 2009
Last Updated on STN: 28 Jan 2009

AB Broad, multispecific CD4(+) and CD8(+) T-cell responses to the hepatitis C

virus (**HCV**), as well as virus-cross-neutralizing antibodies, are associated with recovery from acute infection and may also be associated in chronic **HCV** patients with a favorable response to antiviral treatment. In order to recapitulate all of these responses in an ideal vaccine regimen, we have explored the use of recombinant **HCV** polypeptides combined with various Th1-type adjuvants and replication-defective alphaviral particles encoding **HCV** proteins in various prime/boost modalities in BALB/c mice. Defective chimeric alphaviral particles derived from the Sindbis and Venezuelan equine encephalitis viruses encoding either the **HCV** envelope glycoprotein gpE1/gpE2 heterodimer (E1E2) or nonstructural proteins 3, 4, and 5 (NS345) elicited strong CD8(+) T-cell responses but low CD4(+) T helper responses to these **HCV** gene products. In contrast, recombinant E1E2 glycoproteins adjuvanted with MF59 containing a CpG oligonucleotide elicited strong CD4(+) T helper responses but no CD8(+) T-cell responses. A recombinant NS345 polyprotein also stimulated strong CD4(+) T helper responses but no CD8(+) T-cell responses when adjuvanted with **Iscomatrix** containing CpG. Optimal elicitation of broad CD4(+) and CD8(+) T-cell responses to E1E2 and NS345 was obtained by first priming with Th1-adjuvanted proteins and then boosting with chimeric, defective alphaviruses expressing these **HCV** genes. In addition, this prime/boost regimen resulted in the induction of anti-E1E2 antibodies capable of cross-neutralizing heterologous **HCV** isolates in vitro. This vaccine formulation and regimen may therefore be optimal in humans for protection against this highly heterogeneous global pathogen.

```
=> electronic (w) interaction
L4        4290 ELECTRONIC (W) INTERACTION

=> electronic (w) association
L5           8 ELECTRONIC (W) ASSOCIATION

=> adjuvant
L6      118110 ADJUVANT

=> L6 and L2
L7         227 L6 AND L2

=> L4 and L7
L8           0 L4 AND L7

=> L7 and L5
L9           0 L7 AND L5

=> D L5 IBIB ABS 1-8

L5   ANSWER 1 OF 8  CAPLUS  COPYRIGHT 2009 ACS on STN
```

Full Text | Other References

```
ACCESSION NUMBER:         2008:1295583  CAPLUS
TITLE:                    Automated patent office documentation
INVENTOR(S):              Zellner, Samuel N.
PATENT ASSIGNEE(S):       AT&T Intellectual Property I, L.P., USA
SOURCE:                   U.S.
                          CODEN: USXXAM
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:
```

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 7444589	B2	20081028	US 2004-26790	20041230
PRIORITY APPLN. INFO.:			US 2004-26790	20041230

AB The present disclosure provides systems and methods for automated patent office documentation. Some embodiments provide for analyzing electronic content such as an issued patent, application for patent, Patent and Trademark Office (PTO) office action, associated patent support data such as PTO information, and/or other reference materials, along with user input to identify references to external information, create an **electronic association** to the external information, and insert the **electronic association** into the electronic content.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Cited References

ACCESSION NUMBER: 2008:746167 CAPLUS
DOCUMENT NUMBER: 149:104371
TITLE: Synthesis and Self-Association Properties of Functionalized C3-Symmetric Hexakis(p-substituted-phenylethynyl)triindoles
AUTHOR(S): Garcia-Frutos, Eva M.; Gomez-Lor, Berta
CORPORATE SOURCE: Instituto de Ciencia de Materiales de Madrid, CSIC, Madrid, 28049, Spain
SOURCE: Journal of the American Chemical Society (2008), 130(28), 9173-9177
CODEN: JACSAT; ISSN: 0002-7863
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
OTHER SOURCE(S): CASREACT 149:104371

AB A no. of differently substituted phenylethynyl triindoles has been synthesized by 6-fold Sonogashira coupling in a key step. This new series of hexaalkynyl triindoles self-assoc. through arene-arene interactions in soln. The electronic communication of the external substituents with the central electron-rich triindole core has been demonstrated by means of cyclic voltammetry and optical absorption. A study of the effect of the electronic character of peripheral substituents on their self-assocn. behavior is presented in an effort to shed light on the nature of the π-stacking interactions.

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Cited References

ACCESSION NUMBER: 2007:1154432 CAPLUS
DOCUMENT NUMBER: 147:448160
TITLE: Gene analogue finder: a GRID solution for finding functionally analogous gene products
AUTHOR(S): Tulipano, Angelica; Donvito, Giacinto; Licciulli, Flavio; Maggi, Giorgio; Gisel, Andreas
CORPORATE SOURCE: Dipartimento Interateneo di Fisica, Universita e Politecnico di Bari, Bari, 70126, Italy
SOURCE: BMC Bioinformatics (2007), 8, No pp. given
CODEN: BBMIC4; ISSN: 1471-2105
URL: http://www.biomedcentral.com/content/pdf/1471-

2105-8-329.pdf
PUBLISHER: BioMed Central Ltd.
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
AB To date more than 2,1 million gene products from more than 100000 different species have been described specifying their function, the processes they are involved in and their cellular localization using a very well defined and structured vocabulary, the gene ontol. (GO). Such vast, well defined knowledge opens the possibility of comparing gene products at the level of functionality, finding gene products which have a similar function or are involved in similar biol. processes without relying on the conventional sequence similarity approach. Comparisons within such a large space of knowledge are highly data and computing intensive. For this reason this project was based upon the use of the computational GRID, a technol. offering large computing and storage resources. We have developed a tool, gENe analog fINdEr (ENGINE) that parallelizes the search process and distributes the calcn. and data over the computational GRID, splitting the process into many sub-processes and joining the calcn. and the data on the same machine and therefore completing the whole search in about 3 days instead of occupying one single machine for more than 5 CPU years. The results of the functional comparison contain potential functional analogs for more than 79000 gene products from the most important species. 46% Of the analyzed gene products are well enough described for such an anal. to individuate functional analogs, such as well-known members of the same gene family, or gene products with similar functions which would never have been assocd. by std. methods. ENGINE has produced a list of potential functionally analogous relations between gene products within and between species using, in place of the sequence, the gene description of the GO, thus demonstrating the potential of the GO. However, the current limiting factor is the quality of the assocns. of many gene products from non-model organisms that often have **electronic assocns**., since exptl. information is missing. With future improvements of the GO, this limit will be reduced. ENGINE will manifest its power when it is applied to the whole GODB of more than 2,1 million gene products from more than 100000 organisms. The data produced by this search is planned to be available as a supplement to the GO database as soon as we are able to provide regular updates.
REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Cited References
ACCESSION NUMBER: 2004:300940 CAPLUS
DOCUMENT NUMBER: 140:419575
TITLE: Single-Site Mutation and Secondary Structure Stability: An Isodesmic Reaction Approach. The Case of Unnatural Amino Acid Mutagenesis Ala→Lac
AUTHOR(S): Cieplak, Andrzej Stanislaw; Suermeli, Nur Basak
CORPORATE SOURCE: Department of Chemistry, Bilkent University, Bilkent, Ankara, 06800, Turk.
SOURCE: Journal of Organic Chemistry (2004), 69(10), 3250-3261 CODEN: JOCEAH; ISSN: 0022-3263
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A method is described to evaluate backbone interactions in proteins via computational unnatural amino acid mutagenesis. Several N-acetyl polyalanyl amides (AcAnNH2) were optimized in the representative helical

(310-, 413-, and a "hybrid" κ-helix, n = 7, 9, 10, 14) and hairpin (two- and three-stranded antiparallel β-sheets with type I turns βααε, n = 6, 9, 10) conformations, and extended conformers of N-acetyl polyalanyl methylamides (n = 2, 3) were used to derive multistranded β-sheet fragments. Subsequently, each residue of every model structure was substituted, one at a time, with L-lactic acid. The resulting mutant structures were again optimized, and group-transfer energies ΔEGT were obtained as heats of the isodesmic reactions: AcAnNHR + AcOMe → AcAxLacAyNHR + AcNHMe (R = H, CH3). These group-transfer energies correlate with the degree of charge polarization of the substituted peptide linkages as measured by the difference Δe in H and O Mulliken populations in HN-C:O and with the H-bond distances in the "wild-type" structures. A good correlation obtains for the HF/3-21G and B3LYP/6-31G* group-transfer energies. The destabilization effects are interpreted in terms of loss of interstrand and intrastrand H-bonds, decrease in Lewis basicity of the C:O group, and O···O repulsion. On the basis of several comparisons of Ala → Lac ΔEGT's with heats of the NH → CH2 substitutions, the latter contribution is estd. (B3LYP/6-31G*) to range between 1.5 and 2.4 kcal mol-1, a figure close to the recent exptl. ΔΔG° value of 2.6 kcal mol-1 (McComas, C. C.; Crowley, B. M.; Boger, D. L. J. Am. Chem. Soc. 2003, 125, 9314). The partitioning yields the following max. values of the **electronic assocn**. energy of H-bonds in the examd. sample of model structures (B3LYP/6-31G* ests.): 310-helix De = -1.7 kcal mol-1, α-helix De = -3.8 kcal mol-1, β-sheet De = -6.1 kcal mol-1. The premise of exptl. evaluations of the backbone-backbone H-bonding that Ala → Lac substitution in proteins is isosteric (e.g., Koh, J. T.; Cornish, V. W.; Schultz, P. G. Biochem. 1997, 36, 11314) is often but not always corroborated. Examn. of the integrity of H-bonding pattern and φi, ψi distribution identified several mutants with significant distortions of the "wild-type" structure resulting inter alia from the transitions between i, i + 3 and i, i + 4 H-bonding in helixes, obsd. previously in the crystallog. studies of depsipeptides (Ohyama, T.; Oku, H.; Hiroki, A.; Maekawa, Y.; Yoshida, M.; Katakai, R. Biopolymers 2000, 54, 375; Karle, I. L.; Das, C.; Balaram, P. Biopolymers 2001, 59, 276). Thus, the isodesmic reaction approach provides a simple way to gauge how conformation of the polypeptide chain and dimensions of the H-bonding network affect the strength of backbone-backbone C:O···HN bonds. The results indicate that the stabilization provided by such interactions increases on going from 310-helix to α-helix to β-sheet.

REFERENCE COUNT: 101 THERE ARE 101 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Find References

ACCESSION NUMBER: 2000:318063 CAPLUS
DOCUMENT NUMBER: 133:4306
TITLE: How Strong Is the Cα-H···O:C Hydrogen Bond?
AUTHOR(S): Vargas, Rubicelia; Garza, Jorge; Dixon, David A.; Hay, Benjamin P.
CORPORATE SOURCE: Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA, 99352, USA
SOURCE: Journal of the American Chemical Society (2000), 122(19), 4750-4755

CODEN: JACSAT; ISSN: 0002-7863
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Although the existence of Cα-H···O:C hydrogen bonds in protein structures recently has been established, little is known about their strength and, therefore, the relative importance of these interactions. We have discovered that similar interactions occur in N,N-dimethylformamide dimers. High level ab initio calcns. (MP2/aug-cc-pTZV) yield **electronic assocn.** energies (De) and assocn. enthalpies (ΔH298) for four dimer geometries. These data provide a lower limit of De = -2.1 kcal mol-1 for the Cα-H···O:C hydrogen bond. A linear correlation between C-H···O bond energies and gas-phase proton affinities is reported. The gas-phase anion proton affinity of a peptide Cα-H hydrogen was calcd. (355 kcal mol-1) and used to est. values of De = -4.0 ± 0.5 kcal mol-1 and ΔH298 = -3.0 ± 0.5 kcal mol-1 for the Cα-H···O:C hydrogen bond. The magnitude of this interaction, roughly one-half the strength of the N-H···O:C hydrogen bond, suggests that Cα-H···O:C hydrogen bonding interactions represent a hitherto unrecognized, significant contribution in the detn. of protein conformation.
REFERENCE COUNT: 92 THERE ARE 92 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 8 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

Full Text | Cited References

ACCESSION NUMBER: 2008:45167 BIOSIS
DOCUMENT NUMBER: PREV200800044268
TITLE: Gene analogue finder: a GRID solution for finding functionally analogous gene products.
AUTHOR(S): Tulipano, Angelica; Donvito, Giacinto; Licciulli, Flavio; Maggi, Giorgio; Gisel, Andreas [Reprint Author]
CORPORATE SOURCE: CNR, Ist Tecnol Biomed, Via Amendola 122-D, I-70126 Bari, Italy
angelica.tulipano@ba.infn.it; giacinto.donvito@ba.infn.it; flavio.licciulli@ba.itb.cnr.it; giorgio.maggi@ba.infn.it; andreas.gisel@ba.itb.cnr.it
SOURCE: BMC Bioinformatics, (SEP 3 2007) Vol. 8, pp. Article No.: 329.
ISSN: 1471-2105.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 4 Jan 2008
Last Updated on STN: 4 Jan 2008
AB Background: To date more than 2,1 million gene products from more than 100000 different species have been described specifying their function, the processes they are involved in and their cellular localization using a very well defined and structured vocabulary, the gene ontology (GO). Such vast, well defined knowledge opens the possibility of compare gene products at the level of functionality, finding gene products which have a similar function or are involved in similar biological processes without relying on the conventional sequence similarity approach. Comparisons within such a large space of knowledge are highly data and computing intensive. For this reason this project was based upon the use of the computational GRID, a technology offering large computing and storage resources.Results: We have developed a tool, GENe AnaloGue FINdEr (ENGINE) that parallelizes the search process and distributes the calculation and

data over the computational GRID, splitting the process into many sub-processes and joining the calculation and the data on the same machine and therefore completing the whole search in about 3 days instead of occupying one single machine for more than 5 CPU years. The results of the functional comparison contain potential functional analogues for more than 79000 gene products from the most important species. 46% of the analyzed gene products are well enough described for such an analysis to individuate functional analogues, such as well-known members of the same gene family, or gene products with similar functions which would never have been associated by standard methods.Conclusion: ENGINE has produced a list of potential functionally analogous relations between gene products within and between species using, in place of the sequence, the gene description of the GO, thus demonstrating the potential of the GO. However, the current limiting factor is the quality of the associations of many gene products from non-model organisms that often have **electronic associations**, since experimental information is missing. With future improvements of the GO, this limit will be reduced. ENGINE will manifest its power when it is applied to the whole GODB of more than 2,1 million gene products from more than 100000 organisms. The data produced by this search is planed to be available as a supplement to the GO database as soon as we are able to provide regular updates.

L5 ANSWER 7 OF 8 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

Full Text | More Like This | References

ACCESSION NUMBER: 2004:429038 BIOSIS
DOCUMENT NUMBER: PREV200400429404
TITLE: Single-site mutation and secondary structure stability: An isodesmic reaction approach. The case of unnatural amino acid mutagenesis AlafwdarwLac.
AUTHOR(S): Cieplak, Andrzej Stanislaw [Reprint Author]; Surmeli, Nur Basak
CORPORATE SOURCE: Dept Chem, Bilkent Univ, TR-06800, Ankara, Turkey
cieplak@fen.bilkent.edu.tr
SOURCE: Journal of Organic Chemistry, (May 14 2004) Vol. 69, No. 10, pp. 3250-3261. print.
ISSN: 0022-3263 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 10 Nov 2004
Last Updated on STN: 10 Nov 2004

AB A method is described to evaluate backbone interactions in proteins via computational unnatural amino acid mutagenesis. Several N-acetyl polyalanyl amides (AcAnNH2) were optimized in the representative helical (310-, 413-, and a "hybrid" kappa-helix, n = 7, 9, 10, 14) and hairpin (two- and three-stranded antiparallel beta-sheets with type I turns betaalphaalphamember, n 6, 9, 10) conformations, and extended conformers of N-acetyl polyalanyl methylamides (n 2, 3) were used to derive multistranded beta-sheet fragments. Subsequently, each residue of every model structure was substituted, one at a time, with L-lactic acid. The resulting mutant structures were again optimized, and group-transfer energies DELTAEGT were obtained as heats of the isodesmic reactions: AcAnNHR + AcOMe fwdarw AcAxLacAyNHR + AcNHMe (R = H, CH3). These group-transfer energies correlate with the degree of charge polarization of the substituted peptide linkages as measured by the difference DELTAe in H and O Mulliken populations in HN-C=O and with the H-bond distances in the "wild-type" structures. A good correlation obtains for the HF/3-21G and B3LYP/6-31G* group-transfer energies. The destabilization effects are interpreted in terms of loss of interstrand and intrastrand H-bonds, decrease in Lewis basicity of the C=O group, and OcntdotcntdotcntdotO

repulsion. On the basis of several comparisons of Ala fwdarw Lac DELTAEGT'S with heats of the NH fwdarw CH2 substitutions, the latter contribution is estimated (B3LYP/6-31G*) to range between 1.5 and 2.4 kcal mol-1, a figure close to the recent experimental DELTADELTAGdegree value of 2.6 kcal mol-1 (McComas, C. C.; Crowley, B. M.; Boger, D. L. J. Am. Chem. Soc. 2003, 125, 9314). The partitioning yields the following maximum values of the **electronic association** energy of H-bonds in the examined sample of model structures (B3LYP/6-31G* estimates): 310-helix De = -1.7 kcal mol-1, alpha-helix De = -3.8 kcal mol-1, beta-sheet De = -6.1 kcal mol-1. The premise of experimental evaluations of the backbone-backbone H-bonding that Ala fwdarw Lac substitution in proteins is isosteric (e.g., Koh, J. T.; Cornish, V. W.; Schultz, P. G. Biochemistry 1997, 36, 11314) is often but not always corroborated. Examination of the integrity of H-bonding pattern and phii, psii distribution identified several mutants with significant distortions of the "wild-type" structure resulting inter alia from the transitions between i, i + 3 and i, i + 4 H-bonding in helices, observed previously in the crystallographic studies of depsipeptides (Ohyama, T.; Oku, H.; Hiroki, A.; Maekawa, Y.; Yoshida, M.; Katakai, R. Biopolymers 2000, 54, 375; Karle, I. L.; Das, C.; Balaram, P. Biopolymers 2001, 59, 276). Thus, the isodesmic reaction approach provides a simple way to gauge how conformation of the polypeptide chain and dimensions of the H-bonding network affect the strength of backbone-backbone C=OcntdotcntdotcntdotHN bonds. The results indicate that the stabilization provided by such interactions increases on going from 310-helix to aalphahelix to beta-sheet.

L5 ANSWER 8 OF 8 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

Full Text | Check Availability

ACCESSION NUMBER: 2001:297265 BIOSIS
DOCUMENT NUMBER: PREV200100297265
TITLE: DNA protection from iron-adriamycin-induced oxidative cleavage by the neural hormone melatonin.
AUTHOR(S): Musich, Phillip R. [Reprint author]; Campbell, Sharon E. [Reprint author]; Chua, Balvin H. [Reprint author]
CORPORATE SOURCE: East Tennessee State University, College of Medicine, Johnson City, TN, 37614-0581, USA
SOURCE: FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A512. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001. Orlando, Florida, USA. March 31-April 04, 2001.
CODEN: FAJOEC. ISSN: 0892-6638.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 20 Jun 2001
Last Updated on STN: 19 Feb 2002

AB Adriamycin (ADR), is an effective anti-cancer agent. It is an anthracycline drug with a fused ring system that is planar, hydrophobic and electron rich, features which allow DNA intercalation. Its anti-neoplastic effectiveness stems from its ability to intercalate into DNA and inhibit topoisomerase. ADR also chelates Fe+3 ions and this complex (FeADR (1:2)) oxidatively cleaves DNA via a free radical interaction. As shown by Nohl et al. (1998, Z. Naturforsch, 53c:279-285), enzymes associated specifically with heart mitochondria, increase. ADR free radical formation explaining why it is selectively cardiotoxic. Pretreatment of mice with the neural hormone melatonin eliminates the cardiotoxic effect of ADR therapy without reducing the

drug's antitumor effect (Liu et al. 2000, FASEB J. 14:113.9). The purpose of this study is to analyze the mechanistic features of DNA damage by an Fe+3 ADR (1:2) complex (FeADR) and how melatonin ameliorates this damage. FeADR + glutathione (GSH) cleaves DNA; this oxidative cleavage does not occur with ADR +/- GSH or with FeADR in the absence of GSH. Melatonin reduces this oxidative DNA cleavage by 67%. Mechanistic studies using a supercoiled-to-nicked-circular-conversion assay in conjunction with spectroscopic analyses reveal that: 1) FeADR + GSH forms a reactive intermediate. 2) Melatonin protects the DNA from cleavage by this reactive intermediate. 3) GSH reduction of FeADR diminishes the **electronic association** between the ADR and iron in the complex. 4) FeADR as well as ADR intercalates into DNA. 5) The intercalation of FeADR into DNA alters the rate of oxidative DNA damage. 6) Melatonin also binds to DNA but not by intercalation. These experiments indicate that the cardioprotective effect of melatonin in ADR therapy may stem from melatonin's interaction with a reactive intermediate of FeADR + GSH, and/or a direct DNA interaction. Mechanistic features of this protection by melatonin may involve melatonin-iron interactions or effects on DNA that modify the FeADR intercalation.

=>